```
<!--StartFragment-->RESULT 3
$51398
hypothetical protein YLR260w - yeast (Saccharomyces cerevisiae)
N; Alternate names: hypothetical protein L8479.7
C; Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence revision 12-May-1995 #text change 09-Jul-2004
C:Accession: S51398
R; Miller, N.
submitted to the EMBL Data Library, November 1994
A; Description: The sequence of S. cerevisiae cosmid 8479.
A: Reference number: S51395
A; Accession: S51398
A; Molecule type: DNA
A; Residues: 1-687 <MIL>
A; Cross-references: UNIPROT:Q06147; UNIPARC:UPI000006977B; EMBL:U17244; NID:q577171; PIDN:
AAB67377.1; PID:g577178; GSPDB:GN00012; MIPS:YLR260w
C: Genetics:
A; Gene: SGD: LCB5; MIPS: YLR260w
A; Cross-references: SGD:S0004250
A: Map position: 12R
 Query Match
                     18.5%; Score 356.5; DB 2; Length 687;
 Best Local Similarity 24.9%; Pred. No. 5.6e-24;
 Matches 102; Conservative 76; Mismatches 150; Indels 81; Gaps 11;
          1 VLVLLNPRGGKGKALOLFRSHVOPLLAEAEISFTLMLTERRNHARELVRSEELGRWDALV 60
Qу
            271 IFVIINPFGGKGKAKKLFMTKAKPLLLASRCSIEVVYTKYPGHAIEIAREMDIDKYDTIA 330
Db
         61 VMSGDGLMHEVVNGLMERPDWETAIOK-PLCSLPAGSGNALAASLNHYAGYEQVTNEDLL 119
0.v
             Dh
        331 CASGDGIPHEVINGLYORPDHVKAFNNIAITEIPCGSGNAMSVSC-HW-----TNNP-- 381
        120 TNCTLLLCRRLLSPMNLLSLHTASGLR---LFSVLSLAWGFIADVDLESEKYRRLGEMRF 176
Qy
            Db
        382 SYSTLCLIKSIETRIDLMCCSOPSYAREHPKLSFLSOTYGLIAETDINTEFIRWMGPARF 441
        177 TLGTFLRLAALRTY----- 199
Qу
                 : : 1
                                            .1.1.: :
Db
        442 ELGVAFNIIQKKKYPCEIYVKYAAKSKNELKNHYLEHKNKGSLEFQHITMNKDNEDCDNY 501
        200 --- GRVGSKTPASPVVVOOGPVDAHLV------PLEEPVPSHWTV 235
Ov
                              1:11:
Db
        502 NYENEYETENEDEDEDADADDEDSHLISRDLADSSADOIKEEDFKIKYPLDEGIPSDWER 561
        236 VPDEDFVLVLALLHS----HLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAME 291
Qy
                  Db
        562 L-DPNISNNLGIFYTGKMPYVAADTKFFPAALPSDGTMDMVITDARTSLTRMAPILLGLD 620
        292 KGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVOGOVHP 340
Qy
            621 KGSHVLQ--PEVLHSKILAYKIIPKLGNGLFSVDGEKFPLEPLQVEIMP 667
Db
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